RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _____ 10/785, 116 A

Source: _____ JFW16

Date Processed by STIC: _____ 07/10/2006

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: _10/785, 116A_   CRF Edit Date: _07/10/2006_

Edited by: _DA_

____ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

____ Corrected the SEQ ID NO. Sequence numbers edited were:

_____

____ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

_____

____✓ Deleted: ___ invalid beginning/end-of-file text ; ___ page numbers

____ Inserted mandatory headings/numeric identifiers, specifically:

_____

____ Moved responses to same line as heading/numeric identifier, specifically:

_____

____ Other:

_____
_____
_____

Revised 09/09/2003

RAW SEQUENCE LISTING   DATE: 07/10/2006
PATENT APPLICATION: US/10/785,116A   TIME: 15:28:22

Input Set : A:\PTO.DA.txt
Output Set: N:\CRF4\07072006\J785116A.raw

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  5 <110> APPLICANT: Pecker, Iris
  7         Vlodavsky , Israel
  9         Feinstein, Elena
 13 <120> TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE
ACTIVITY AND
 14         EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS
 18 <130> FILE REFERENCE: 27674
C--> 21 <140> CURRENT APPLICATION NUMBER: US/10/785,116A
C--> 21 <141> CURRENT FILING DATE: 2004-02-25
 21 <160> NUMBER OF SEQ ID NOS: 49
 25 <170> SOFTWARE: PatentIn version 3.1
 29 <210> SEQ ID NO: 1
 31 <211> LENGTH: 27
 33 <212> TYPE: DNA
 35 <213> ORGANISM: Artificial sequence
 39 <220> FEATURE:
 41 <223> OTHER INFORMATION: Synthetic oligonucleotide
 43 <400> SEQUENCE: 1
 44 ccatcctaat acgactcact atagggc                                    27
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 53 <213> ORGANISM: Artificial sequence
 57 <220> FEATURE:
 59 <223> OTHER INFORMATION: Synthetic oligonucleotide
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 65 <210> SEQ ID NO: 3
 67 <211> LENGTH: 23
 69 <212> TYPE: DNA
 71 <213> ORGANISM: Artificial sequence
 75 <220> FEATURE:
 77 <223> OTHER INFORMATION: Synthetic oligonucleotide
 79 <400> SEQUENCE: 3
 80 actcactata gggctcgagc ggc                                        23
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 85 <211> LENGTH: 22
 87 <212> TYPE: DNA
 89 <213> ORGANISM: Artificial sequence
 93 <220> FEATURE:
 95 <223> OTHER INFORMATION: Synthetic oligonucleotide
 97 <400> SEQUENCE: 4
 98 gcatcttagc cgtctttctt cg                                         22
101 <210> SEQ ID NO: 5
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RAW SEQUENCE LISTING   DATE: 07/10/2006
PATENT APPLICATION: US/10/785,116A   TIME: 15:28:22

Input Set : A:\PTO.DA.txt
Output Set: N:\CRF4\07072006\J785116A.raw

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107 <213> ORGANISM: Artificial sequence
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113 <223> OTHER INFORMATION: Synthetic oligonucleotide
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121 <211> LENGTH: 23
123 <212> TYPE: DNA
125 <213> ORGANISM: Artificial sequence
129 <220> FEATURE:
131 <223> OTHER INFORMATION: Synthetic oligonucleotide
133 <400> SEQUENCE: 6
134 ttcgatccca agaaggaatc aac                                      23
137 <210> SEQ ID NO: 7
139 <211> LENGTH: 24
141 <212> TYPE: DNA
143 <213> ORGANISM: Artificial sequence
147 <220> FEATURE:
149 <223> OTHER INFORMATION: Synthetic oligonucleotide
151 <400> SEQUENCE: 7
152 gtagtgatgc catgtaactg aatc                                     24
155 <210> SEQ ID NO: 8
157 <211> LENGTH: 9
159 <212> TYPE: PRT
161 <213> ORGANISM: Artificial sequence
165 <220> FEATURE:
167 <223> OTHER INFORMATION: Peptide derived from tryptic digestion of human heparenase
169 <400> SEQUENCE: 8
171 Tyr Gly Pro Asp Val Gly Gln Pro Arg
172 1               5
175 <210> SEQ ID NO: 9
177 <211> LENGTH: 1721
179 <212> TYPE: DNA
181 <213> ORGANISM: Homo sapiens
185 <400> SEQUENCE: 9
186 ctagagcttt cgactctccg ctgcgcggca gctggcgggg ggagcagcca ggtgagccca      60
188 agatgctgct gcgctcgaag cctgcgctgc cgccgccgct gatgctgctg ctcctggggc     120
190 cgctgggtcc cctctcccct ggcgccctgc cccgacctgc gcaagcacag gacgtcgtgg     180
192 acctggactt cttcacccag gagccgctgc acctggtgag cccctcgttc ctgtccgtca     240
194 ccattgacgc caacctggcc acggacccgc ggttcctcat cctcctgggt tctccaaagc     300
196 ttcgtacctt ggccagaggc ttgtctcctg cgtacctgag gtttggtggc accaagacag     360
198 acttcctaat tttcgatccc aagaaggaat caacctttga agagagaagt tactggcaat     420
200 ctcaagtcaa ccaggatatt tgcaaatatg gatccatccc tcctgatgtg gaggagaagt     480
202 tacggttgga atggccctac caggagcaat gctactccg agaacactac cagaaaaagt     540
204 tcaagaacag cacctactca agaagctctg tagatgtgct atacactttt gcaaactgct     600
206 caggactgga cttgatcttt ggcctaaatg cgttattaag aacagcagat ttgcagtgga     660
208 acagttctaa tgctcagttg ctcctggact actgctcttc caaggggtat aacatttctt     720
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210 gggaactagg caatgaacct aacagtttcc ttaagaaggc tgatattttc atcaatgggt    780
212 cgcagttagg agaagattat attcaattgc ataaacttct aagaaagtcc accttcaaaa    840
214 atgcaaaact ctatggtcct gatgttggtc agcctcgaag aaagacggct aagatgctga    900
216 agagcttcct gaaggctggt ggagaagtga ttgattcagt tacatggcat cactactatt    960
218 tgaatggacg gactgctacc agggaagatt ttctaaaccc tgatgtattg gacatttta    1020
220 tttcatctgt gcaaaaagtt ttccaggtgg ttgagagcac caggcctggc aagaaggtct    1080
222 ggttaggaga acaagctct gcatatggag gcggagcgcc cttgctatcc gacacctttg    1140
224 cagctggctt tatgtggctg gataaattgg gcctgtcagc ccgaatggga atagaagtgg    1200
226 tgatgaggca agtattcttt ggagcaggaa actaccattt agtggatgaa aacttcgatc    1260
228 ctttacctga ttattggcta tctcttctgt tcaagaaatt ggtgggcacc aaggtgttaa    1320
230 tggcaagcgt gcaaggttca aagagaagga agcttcgagt atacctcat tgcacaaaca    1380
232 ctgacaatcc aaggtataaa gaaggagatt taactctgta tgccataaac ctccataacg    1440
234 tcaccaagta cttgcggtta ccctatcctt tttctaacaa gcaagtggat aaataccttc    1500
236 taagaccttt gggacctcat ggattacttt ccaaatctgt ccaactcaat ggtctaactc    1560
238 taaagatggt ggatgatcaa accttgccac ctttaatgga aaaacctctc cggccaggaa    1620
240 gttcactggg cttgccagct ttctcatata gtttttttgt gataagaaat gccaaagttg    1680
242 ctgcttgcat ctgaaaataa aatatactag tcctgacact g                        1721
246 <210> SEQ ID NO: 10
248 <211> LENGTH: 543
250 <212> TYPE: PRT
252 <213> ORGANISM: Homo sapiens
256 <400> SEQUENCE: 10
258 Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu Leu
259 1               5                   10                  15
262 Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg Pro
263             20                  25                  30
266 Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu Pro
267         35                  40                  45
270 Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn
271     50                  55                  60
274 Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu
275 65                  70                  75                  80
278 Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly
279             85                  90                  95
282 Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr Phe
283             100                 105                 110
286 Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys Lys
287         115                 120                 125
290 Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu Trp
291     130                 135                 140
294 Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys Phe
295 145                 150                 155                 160
298 Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe
299             165                 170                 175
302 Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu
303             180                 185                 190
306 Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu
307         195                 200                 205
310 Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn
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RAW SEQUENCE LISTING   DATE: 07/10/2006
PATENT APPLICATION: US/10/785,116A   TIME: 15:28:22

Input Set : A:\PTO.DA.txt
Output Set: N:\CRF4\07072006\J785116A.raw

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311     210                  215                  220
314 Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser
315 225                 230                  235                  240
318 Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys Leu Leu Arg Lys Ser
319                 245                  250                  255
322 Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg
323         .       260                  265                  270
326 Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu
327             275                  280                  285
330 Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg Thr
331     290                  295                  300
334 Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe Ile
335 305                 310                  315                  320
338 Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro Gly
339                 325                  330                  335
342 Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly Ala
343             340                  345                  350
346 Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys
347         355                  360              365
350 Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln Val
351     370                  375                  380
354 Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp Pro
355 385                 390                  395                  400
358 Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly Thr
359             405                  410                  415
362 Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu Arg
363             420                  425                  430
366 Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu Gly
367         435                  440                  445
370 Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr Leu
371     450                  455                  460
374 Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu Leu
375 465                 470                  475                  480
378 Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu Asn
379             485                  490                  495
382 Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu Met
383         500                  505                  510
386 Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe Ser
387         515                  520                  525
390 Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile
391     530                  535                  540
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395 <210> SEQ ID NO: 11
397 <211> LENGTH: 1721
399 <212> TYPE: DNA
401 <213> ORGANISM: Homo sapiens
405 <220> FEATURE:
407 <221> NAME/KEY: CDS
409 <222> LOCATION: (63)..(1691)
411 <223> OTHER INFORMATION:

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    418 ag atg ctg ctg cgc tcg aag cct gcg ctg ccg ccg ccg ctg atg ctg          107
    419    Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu
    420    1               5                   10                  15
    422 ctg ctc ctg ggg ccg ctg ggt ccc ctc tcc cct ggc gcc ctg ccc cga        155
    423 Leu Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg
    424                 20                  25                  30
    426 cct gcg caa gca cag gac gtc gtg gac ctg gac ttc ttc acc cag gag        203
    427 Pro Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu
    428             35                  40                  45
    430 ccg ctg cac ctg gtg agc ccc tcg ttc ctg tcc gtc acc att gac gcc        251
    431 Pro Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala
    432         50                  55                  60
    434 aac ctg gcc acg gac ccg cgg ttc ctc atc ctc ctg ggt tct cca aag        299
    435 Asn Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys
    436         65                  70                  75
    438 ctt cgt acc ttg gcc aga ggc ttg tct cct gcg tac ctg agg ttt ggt        347
    439 Leu Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly
    440 80                  85                  90                  95
    442 ggc acc aag aca gac ttc cta att ttc gat ccc aag aag gaa tca acc        395
    443 Gly Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr
    444                 100                 105                 110
    446 ttt gaa gag aga agt tac tgg caa tct caa gtc aac cag gat att tgc        443
    447 Phe Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys
    448             115                 120                 125
    450 aaa tat gga tcc atc cct cct gat gtg gag gag aag tta cgg ttg gaa        491
    451 Lys Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu
    452             130                 135                 140
    454 tgg ccc tac cag gag caa ttg cta ctc cga gaa cac tac cag aaa aag        539
    455 Trp Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys
    456         145                 150                 155
    458 ttc aag aac agc acc tac tca aga agc tct gta gat gtg cta tac act        587
    459 Phe Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr
    460 160                 165                 170                 175
    462 ttt gca aac tgc tca gga ctg gac ttg atc ttt ggc cta aat gcg tta        635
    463 Phe Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu
    464                 180                 185                 190
    466 tta aga aca gca gat ttg cag tgg aac agt tct aat gct cag ttg ctc        683
    467 Leu Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu
    468             195                 200                 205
    470 ctg gac tac tgc tct tcc aag ggg tat aac att tct tgg gaa cta ggc        731
    471 Leu Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly
    472             210                 215                 220
    474 aat gaa cct aac agt ttc ctt aag aag gct gat att ttc atc aat ggg        779
    475 Asn Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly
    476         225                 230                 235
    478 tcg cag tta gga gaa gat tat att caa ttg cat aaa ctt cta aga aag        827
    479 Ser Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys Leu Leu Arg Lys
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 07/10/2006
PATENT APPLICATION: US/10/785,116A   TIME: 15:28:23

Input Set : **A:\PTO.DA.txt**
Output Set: **N:\CRF4\07072006\J785116A.raw**

<u>Please Note:</u>
**Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.**

Seq#:47; N Pos. 507
Seq#:49; Xaa Pos. 9

VERIFICATION SUMMARY   DATE: 07/10/2006
PATENT APPLICATION: **US/10/785,116A**   TIME: 15:28:23

Input Set : **A:\PTO.DA.txt**
Output Set: **N:\CRF4\07072006\J785116A.raw**

```
L:21 M:270 C: Current Application Number differs, Replaced Current Application No
L:21 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:415 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:411
L:855 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:851
L:3270 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:45,Line#:3266
L:3499 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47 after pos.:480
L:3555 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49 after pos.:0
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Raw Sequence Listing before editing (for reference only)

IFW16

RAW SEQUENCE LISTING   DATE: 07/06/2006
PATENT APPLICATION: US/10/785,116A   TIME: 17:02:17

Input Set : A:\PTO.KD.txt
Output Set: N:\CRF4\07062006\J785116A.raw

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    5 <110> APPLICANT: Pecker, Iris
    7         Vlodavsky , Israel
    9         Feinstein, Elena
   13 <120> TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE
ACTIVITY AND
   14         EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS
   18 <130> FILE REFERENCE: 27674
C--> 21 <140> CURRENT APPLICATION NUMBER: US/10/785,116A
C--> 21 <141> CURRENT FILING DATE: 2004-02-25
   21 <160> NUMBER OF SEQ ID NOS: 49
   25 <170> SOFTWARE: PatentIn version 3.1
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Does Not Comply
Corrected Diskette Needed

$C\rho\xi$-1)

ERRORED SEQUENCES

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 3542 <210> SEQ ID NO: 49
 3543 <211> LENGTH: 44
 3544 <212> TYPE: PRT
 3545 <213> ORGANISM: Rattus norvegicus
 3548 <220> FEATURE:
 3549 <221> NAME/KEY: misc_feature
 3550 <222> LOCATION: (9)..(9)
 3551 <223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
 3553 <400> SEQUENCE: 49
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     3556 1               5                   10                  15
     3559 Leu Pro Ala Gly Ser Ser Leu Ser Val Pro Ala Phe Ser Tyr Gly Phe
     3560             20                  25                  30
     3563 Phe Val Ile Arg Asn Ala Lys Ile Ala Ala Cys Ile
     3564             35                  40
E--> 3569 44
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deleted

VERIFICATION SUMMARY   DATE: 07/06/2006
PATENT APPLICATION: **US/10/785,116A**   TIME: 17:02:18

Input Set : **A:\PTO.KD.txt**
Output Set: **N:\CRF4\07062006\J785116A.raw**

L:21 M:270 C: Current Application Number differs, Replaced Current Application No
L:21 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:415 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:411
L:855 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:851
L:3270 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:45,Line#:3266
L:3499 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47 after pos.:480
L:3555 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49 after pos.:0
L:3569 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:49